Appl. No.: Continuation of 10/032,307
Amdt. dated September 26, 2003

PATENT

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

Claims 1-109 (Canceled).

Claim 110.   (New) A thermodynamic method for predicting duplex stability of an oligonucleotide sequence comprising at least one modified nucleotide base, said method comprising:

a) providing an oligonucleotide having a sequence of N bases, wherein said oligonucleotide comprises at least one modified base; and

b) calculating duplex stability of said oligonucleotide using an algorithm applying a nearest-neighbor model for duplex formation thermodynamics for each of the N-1 neighboring base pairs, each nearest neighbor thermodynamic parameter defining a thermodynamic contribution of two corresponding neighboring bases.

Claim 111.   (New) A method for predicting the melting temperature (T_m) of an oligonucleotide sequence comprising at least one modified nucleotide base, said method comprising:

a) providing an oligonucleotide having a sequence of N bases, wherein said oligonucleotide comprises at least one modified base; and

b) calculating a melting temperature (T_m) of said oligonucleotide using an algorithm applying nearest neighbor thermodynamic parameters for each of the N-1 neighboring base pairs, each nearest neighbor thermodynamic parameter defining a thermodynamic contribution of two corresponding neighboring bases.

Claim 112.   (New) The method of any one of claims 110 or 111, wherein said oligonucleotide sequence is derived from a database source.

Claim 113.   (New) The method of claim 112, wherein said oligonucleotide sequence is derived from Genbank.

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Claim 114.   (New) The method of any one of claims 110 or 111, wherein said at least one modified base is a member selected from the group consisting of a base attached to an amino acid, a polyamide nucleic acid (PNA) and a locked nucleic acid sugar.

Claim 115.   (New) The method of claim 114, wherein said modified base is attached to PNA.

Claim 116.   (New) The method of claim 114, wherein said modified base a locked nucleic acid sugar.
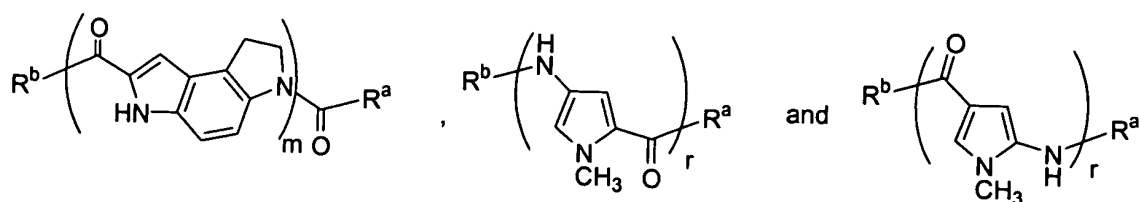
Claim 117.   (New) The method of any one of claims 110, 111, 115 or 116, wherein said oligonucleotide comprising at least one modified base has superior mismatch discrimination, in comparison to unmodified nucleotides.

Claim 118.   (New) The method of any one of claims 110 or 111, wherein said at least one modified base is a member selected from the group consisting of a universal base, PPA, PPG, PPPA, PPPG, PU, PC, HOPU, HOBuU, HOBuC, $(NH_2)_2PPPA$, $(NH_2)_2PPPAOH$, $(NH_2)_2BuPPAOH$, $(NH_2)_2PPAI$, and HOBuPPG.

Claim 119.   (New) The method of any one of claims 110 or 111, wherein said oligonucleotide has attached to it one or more members selected from the group consisting of a minor groove binder, a fluorophore and a quencher.

Claim 120.   (New) The method of claim 119, wherein said oligonucleotide sequence has a minor groove binder attached thereto.

Claim 121.   (New) The method of claim 120, wherein said minor groove binder has a formula selected from the group consisting of:

wherein

the subscript m is an integer of from 2 to 5;

the subscript r is an integer of from 2 to 10; and

each R^a and R^b is independently a linking group to said modified oligonucleotide, H, OR^c, NR^cR^d, $COOR^c$ and $-CONR^cR^d$ wherein each R^c and R^d is selected from the group consisting of H, (C_1-C_{12})heteroalkyl, (C_2-C_{12})heteroalkenyl, (C_2-C_{12})heteroalkynyl, (C_1-C_{12})alkyl, (C_2-C_{12})alkenyl, (C_2-C_{12})alkynyl, aryl(C_1-C_{12})alkyl and aryl.

Claim 122. (New) The method of claim 120, wherein said minor groove binder is attached to the oligonucleotide via a quencher molecule.

Claim 123. (New) The method of any one of claims 110 or 111, wherein said algorithm predicts the melting temperature (T_m) of said oligonucleotide with an accuracy of about +/- 2°C.

Claim 124. (New) The method of any one of claims 110 or 111, wherein said method is applied in establishing appropriate conditions for hybridization, renaturation, mapping variations of base compositions of sequences or determination of sequence complexity and divergence.

Claim 125. (New) The method of any one of claims 110 or 111, wherein said oligonucleotide is a capture probe in an array.